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| **Parameter** | **AGO-OVAR 11** | **Data on original studies included to the meta analyses by Riester et al., Liu et al. and Tucker et al.** |
| % of patients w vs w/o complete resection | N=104 RD0 and N=162 RD>0 | 1. N=257 RD≤1 vs N=264 RD>1  2. N=13 RD0 and N=41 RD>0  3. N= 22 RD0 vs N=21 RD<2 cm vs N=109 RD>2 cm  4. N=57 RD ≤1 and N=53 RD>1  5. N=95 RD ≤1 and N=22 RD>1  6. N=71 RD ≤1 and N=29 RD>1  7. N=92 RD ≤1 and N=93 RD>1  8. N=64 RD ≤1 and N=16 RD>1  9. N=103 RD ≤1 and N=157 RD>1  10. N=68 RD0 and N=164 RD>0  11. N=63 RD ≤1 and N=56 RD>1  12. N=223 RD0 vs N=342 RD>0 |
| Location of tumor sample collection | not reported | 1.-12. not reported |
| Frozen/ FFPE | FFPE | 1. FFPE  2. fresh frozen  3. fresh frozen  4. fresh frozen  5. fresh frozen and FFPE  6. fresh frozen  7. fresh frozen  8. not reported  9. fresh frozen  10. fresh frozen  11. fresh frozen  12. fresh frozen |
| Quality features tumor vs. stroma | >70% tumor | 1. selected areas for sampling were based on having low levels of infiltrating, necrotic, or other contaminating non-tumor tissue.  2. ≥50% tumor  3. median percentage tumor cells: 70%, interquartile range: 50%–80%  4. > 80% of tumor cells  5. microdissection of from 5,000 dissected tumor cells  6. not reported  7. ≥80% tumor  8. ≥75% cancer cells  9. > 70% tumor cells  10. 92.5% ≥50% tumor; 7.5% tumor 30%-49%  11. > 70% tumor cells  12. 70% tumor cell nuclei with less than 20% necrosis |
| Determination of residual disease | surgeon at the end of surgery | 1.-11. not reported  12. surgeon at the end of surgery |
| Gene expression analyses platform | Whole-Genome DASL HT assay with the HumanRef-8 Bead Chip | 1. Illumina HumanRef-8 v2  2. Custom made  3. Operon Human v3  4. Agilent G4112a  5. Affymetrix U133 Plus 2.0  6. Affymetrix U95 v  7. Affymetrix U133A  8. TaqManqRT-PCR  9. Agilent G4112a  10. Affymetrix U133 Plus  11. Affymetrix U133a  12. Affymetrix HT U133a |

Supplement Table 1: Description of the resource data of the meta analyses conducted by Riester et al., Liu et.al. and Tucker et al. in comparison to the AGO-OVAR 11/ ICON 7 samples; 1. Bentink et al. [[34](#_ENREF_34)]; 2. Partheen et al.[[35](#_ENREF_35)]; 3. Crijns et al. [[36](#_ENREF_36)]; 4. Yoshihara et al. [[37](#_ENREF_37)]; 5. Mok et al. [[38](#_ENREF_38)]; 6. Konstantinopoulos et al. [[39](#_ENREF_39)]; 7. Bonome et al. [[40](#_ENREF_40)]; 8. Gillet et al. [[41](#_ENREF_41)]; 9. Yoshihara et al. [[42](#_ENREF_42)]; 10. Tothill et al. [[43](#_ENREF_43)]; 11. Dressman et al. [[44](#_ENREF_44)]; 12. TCGA [[18](#_ENREF_18)]; Liu et al. undertook a meta analyses including 7., 10. and 12; Tucker et al. undertook a meta analyses of 10. and 12. TCGA.